US09652282.txt	
(1) GENERAL INFORMATION:	
(i) APPLICANT: Gately, Maurice K.	
Presky, David H.	
(ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12	
(iii) NUMBER OF SEQUENCES: 4	
(iv) CORRESPONDENCE ADDRESS:	
(A) ADDRESSEE: Hoffmann-La Roche Inc.	
(B) STREET: 340 Kingsland Street	
(C) CITY: Nutley	
(D) STATE: New Jersey	
(E) COUNTRY: United States	
(F) ZIP: 07110-1199	
(v) COMPUTER READABLE FORM:	
(A) MEDIUM TYPE: Floppy disk	
(B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS	
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25	
(vi) CURRENT APPLICATION DATA:	
(A) APPLICATION NUMBER: US/09/652,282	
(B) FILING DATE: 30-Aug-2000	
(C) CLASSIFICATION: <unknown></unknown>	
(vii) PRIOR APPLICATION DATA:	
(A) APPLICATION NUMBER: 09/232,522	
(B) FILING DATE: <unknown></unknown>	
(viii) ATTORNEY/AGENT INFORMATION:	
(A) NAME: Buchholz, Briana C.	
(B) REGISTRATION NUMBER: 39,123	
(C) REFERENCE/DOCKET NUMBER: CD 1048P	
(ix) TELECOMMUNICATION INFORMATION:	
(A) TELEPHONE: 973-235-6208	
(B) TELEFAX: 973-235-2363	
(2) INFORMATION FOR SEQ ID NO: 1:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 321 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(jii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: mouse	
(G) CELL TYPE: Hybridoma	
(H) CELL LINE: HIL-12F3-16G2	
(ix) FEATURE:	
(A) NAME/KEY: CDS	
(B) LOCATION: 1321	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	4.0
CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC	48
Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser 1 15	
CTC ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC	0.6
Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn	96
20 25 30	
TGG ATC CGG AAA TTC CCA GGG AAT AAA TTT GAG TAC ATG GGA TTC ATA	144
Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile	144
35 40 45	
AGT TAT AGT GGT AGC ACT TAC AAT AAT CCA TCT CTC AAA AAT CGA GTC	192
Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val	192
50 55 60	•
TCC ATC ACT CGA GAC ACA TCC AAT AAC CAG TAC TAC CTG CAG TTG AGT	240
Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser	210
65 70 75 80	

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								U:	5096	52282	2.tx	t					
							TCA Ser										288
							GGC Gly										321
(2)	(i)	SEQUENT (A)	JENCI ) LEI ) TYI ) TOI	E CHANGTH PE: 6	ARAC : 10 amin GY:	TERI: 7 am 0 ac 1ine:	STIC: ino a id ar	S:	5								
		SEQ	JENCI	E DES	SCRI	PTIO		EQ II Leu	O NO Val	Lys	Pro	Ser	Gln	Thr		Ser	
	Leu	Thr	Cys	Ser 20	۷al	Thr	Glу	Asp	Ser 25	lle	Thr	Ser	Gly	Tyr	Trp	Asn	
	Trp	Ile	Arg		Phe	Pro	Glу	Asn 40		Phe	Glu	Tyr	Met 45	Gly	Phe	Ile	
	Ser	Tyr 50	Ser	Gly	Ser	Thr	Tyr 55	. •	Asn	Pro	Ser	Leu 60		Asn	Arg	٧a٦	
	Ser 65	Ile	Thr	Arg	Asp	Thr 70	Ser	Asn	Asn	Gln	Tyr 75		Leu	Gln	Leu	Ser 80	
	Ser	٧a٦	Thr	Thr	Glu 85	Asp	Ser	Ala	Thr	Tyr 90	Tyr	Cys	Ala	Arg	Ser 95		
	Asp	Ala	Leu	Asp 100	Tyr	Trp	Gly	Ala	Gly 105	Thr	Thr						
	(ii) (iii) (iv) (vi) (ix)	(A) (B) (C) (D) (D) MOLE HYPO ANT: ORIO (A) (G) (H) FEA (B) SEQU	) LEN ) TYI ) TYI ) TOI ECULI DTHE C-SEN GINAL ) ORC ) CEL (URE: ) NAN ) LOC UJENCE	NGTH PE: IR RANDIPOLOGE TYI FICAI NSE: SOU SANIS LL TY LL LI HE/KI CATICE DES	: 300 nucle EDNE: GY: PE: ( NO URCE SM: ( YPE: INE: EY: ( ON: [ SCRII	8 baseic assistance SS: Glinea CDNA CDNA Hybrid HIL- CDS 130 PTION	doub ar e ridor -12F: 06 N: SI	airs le ma 3-200	O NO:	: _3:							
	Glu 1	Glu	Ser	Gly	Pro 5	Ser	CTC Leu	val	Lys	Pro 10	Ser	Gln	Thr	Leu	Ser 15	Leu	48
	ACC Thr	TGT Cys	TCT Ser	GTC Val 20	ACT Thr	GGC Gly	GAC Asp	TCC Ser	ATC Ile 25	ACC Thr	AGT Ser	GGT Gly	TAC Tyr	TGG Trp 30	AAC Asn	TGG Trp	96
	ATC Ile	CGG Arg	AAA Lys 35	TTC Phe	CCA Pro	GAT Asp	AAT Asn	ACA Thr 40	CTT	GAG Glu	TAC Tyr	ATG Met	GGA Gly	TAC	ATA Ile	AGT Ser	144
	TAC Tyr	AGT Ser 50	GGT	AGT Ser	ACT Thr	TAC Tyr	TAC Tyr	AAT	CCA Pro	TCT Ser	CTC Leu	AGA Arg	AGT Ser	CGA Arg	ATC Ile	TCC Ser	192
	ATC Ile 65	ACT	CGA Arg	GAC Asp	ACA Thr	TCC Ser 70	AAG Lys	AAC Asn	CAG Gln	TAC Tyr	TCC Ser 75	ATG Met	CAG Gln	TTG Leu	AAT Asn	TCT Ser 80	240
	GTG	ACT Thr	ACT Thr	GAG Glu	GAC Asp	ACA	GCC Ala	ACA Thr	Tyr	TAC Tyr	TGT Cys	GCA Ala	AGA Arg	TCC Ser	TCG Ser	GAT	288

D

308

GCT ATG GAC TAC TGG GGC GC Ala Met Asp Tyr Trp Gly 100

(2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu 10 15 Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp 20 25 30 Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser 50 55 60 Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser 65 70 75 80 Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp 85 90 95 Ala Met Asp Tyr Trp Gly
100

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